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OFFICE OF PETITIONS



1600

## RAW SEQUENCE LISTING

DATE: 04/21/2004

PATENT APPLICATION: US/09/933,915A

TIME: 07:09:44

Input Set : A:\07917-120001.txt

Output Set: N:\CRF4\04212004\I933915A.raw

4 <110> APPLICANT: Odgren, Paul R.  
5 Marks, Sandy C.  
6 Choi, Yongwon  
8 <120> TITLE OF INVENTION: TRANCE REGULATION OF CHONDROCYTE  
9 DIFFERENTIATION  
11 <130> FILE REFERENCE: 07917-120001  
13 <140> CURRENT APPLICATION NUMBER: 09/933,915A  
14 <141> CURRENT FILING DATE: 2001-08-20  
16 <150> PRIOR APPLICATION NUMBER: 60/226,197  
17 <151> PRIOR FILING DATE: 2000-08-18  
19 <160> NUMBER OF SEQ ID NOS: 19  
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
23 <210> SEQ ID NO: 1  
24 <211> LENGTH: 2226  
25 <212> TYPE: DNA  
26 <213> ORGANISM: Homo sapiens  
28 <220> FEATURE:  
29 <221> NAME/KEY: CDS  
30 <222> LOCATION: (157)...(1107)  
32 <400> SEQUENCE: 1

33 ctcgacccac gcgctccgcgc gccccaggag ccaaagccgg gctccaagtc ggcgccccac 60  
34 gtcgaggctc cgccgcagcc tccggagttg gccgcagaca agaaggggag ggagcgggag 120  
35 agggaggaga gctccgaagc gagagggccg agcgcc atg cgc cgc gcc agc aga 174  
36 Met Arg Arg Ala Ser Arg  
37 1 5  
39 gac tac acc aag tac ctg cgt ggc tcg gag gag atg ggc ggc ggc ccc 222  
40 Asp Tyr Thr Lys Tyr Leu Arg Gly Ser Glu Glu Met Gly Gly Gly Pro  
41 10 15 20  
43 gga gcc ccg cac gag ggc ccc ctg cac gcc ccg ccg ccg cct gcg ccg 270  
44 Gly Ala Pro His Glu Gly Pro Leu His Ala Pro Pro Pro Pro Ala Pro  
45 25 30 35  
47 cac cag ccc ccc gcc gcc tcc cgc tcc atg ttc gtg gcc ctc ctg ggg 318  
48 His Gln Pro Pro Ala Ala Ser Arg Ser Met Phe Val Ala Leu Leu Gly  
49 40 45 50  
51 ctg ggg ctg ggc cag gtt gtc tgc agc gtc gcc ctg ttc ttc tat ttc 366  
52 Leu Gly Leu Gly Gln Val Val Cys Ser Val Ala Leu Phe Phe Tyr Phe  
53 55 60 65 70  
55 aga gcg cag atg gat cct aat aga ata tca gaa gat ggc act cac tgc 414  
56 Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys  
57 75 80 85  
59 att tat aga att ttg aga ctc cat gaa aat gca gat ttt caa gac aca 462  
60 Ile Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr  
61 90 95 100

P.6  
ENTERED

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```

63 act ctg gag agt caa gat aca aaa tta ata cct gat tca tgt agg aga      510
64 Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg
65      105      110      115
67 att aaa cag gcc ttt caa gga gct gtg caa aag gaa tta caa cat atc      558
68 Ile Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile
69      120      125      130
71 gtt gga tca cag cac atc aga gca gag aaa gcg atg gtg gat ggc tca      606
72 Val Gly Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser
73 135      140      145      150
75 tgg tta gat ctg gcc aag agg agc aag ctt gaa gct cag cct ttt gct      654
76 Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala
77      155      160      165
79 cat ctc act att aat gcc acc gac atc cca tct ggt tcc cat aaa gtg      702
80 His Leu Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val
81      170      175      180
83 agt ctg tcc tct tgg tac cat gat cgg ggt tgg gcc aag atc tcc aac      750
84 Ser Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn
85      185      190      195
87 atg act ttt agc aat gga aaa cta ata gtt aat cag gat ggc ttt tat      798
88 Met Thr Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr
89      200      205      210
91 tac ctg tat gcc aac att tgc ttt cga cat cat gaa act tca gga gac      846
92 Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp
93 215      220      225      230
95 cta gct aca gag tat ctt caa cta atg gtg tac gtc act aaa acc agc      894
96 Leu Ala Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser
97      235      240      245
99 atc aaa atc cca agt tct cat acc ctg atg aaa gga gga agc acc aag      942
100 Ile Lys Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys
101      250      255      260
103 tat tgg tca ggg aat tct gaa ttc cat ttt tat tcc ata aac gtt ggt      990
104 Tyr Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly
105      265      270      275
107 gga ttt ttt aag tta cgg tct gga gag gaa atc agc atc gag gtc tcc      1038
108 Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser
109      280      285      290
111 aac ccc tcc tta ctg gat ccg gat cag gat gca aca tac ttt ggg gct      1086
112 Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala
113 295      300      305      310
115 ttt aaa gtt cga gat ata gat tgagccccag tttttggagt gttatgtatt      1137
116 Phe Lys Val Arg Asp Ile Asp
117      315
119 tcctggatgt ttggaacat tttttaaaac aagccaagaa agatgtatat aggtgtgtga      1197
120 gactactaag aggcattggcc ccaacggtac acgactcagt atccatgctc ttgaccttgt      1257
121 agagaacacg cgtattttaca gccagtggga gatgttagac tcatgggtgtg ttacacaatg      1317
122 gttttttaaat tttgtaatga attcctagaa ttaaacacaga ttggagcaat tacgggttga      1377
123 ccttatgaga aactgcatgt gggctatggg aggggttggc ccctggteat gtgcccccttc      1437
124 gcagctgaag tggagagggt gtcattctagc gcaattgaag gatcatctga aggggcaaat      1497
125 tcttttgaat tgttacatca tgctggaacc tgcaaaaaat actttttcta atgaggagag      1557

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```

126 aaaatatatg tttttttata taatatctaa agttatatatt cagatgtaat gttttctttg 1617
127 caaagtattg taaattatat ttgtgctata gtatttgatt caaaatattt aaaaatgtct 1677
128 tgctgttgac atatttaatg ttttaaagt acagacatat ttaactggtg cactttgtaa 1737
129 attccctggg gaaaacttgc agctaaggag gggaaaaaaa tgttgtttcc taatatcaaa 1797
130 tgcagtatat ttcttcgttc tttttaagtt aatagatttt ttcagacttg tcaagcctgt 1857
131 gcaaaaaaat taaaatggat gccttgaata ataagcagga tgttggccac caggtgcctt 1917
132 tcaaatttag aaactaattg acttttagaaa gctgacattg ccaaaaagga tacataatgg 1977
133 gccactgaaa tctgtcaaga gtagttatat aattgttgaa caggtgtttt tccacaagtg 2037
134 ccgcaaattg tacctttttt tttttttcaa aatagaaaag ttattagtgg tttatcagca 2097
135 aaaaagtcca attttaattt agtaaagtgt atcttatact gtacaataaa aacattgcct 2157
136 ttgaatgtta attttttggg acaaaaaataa atttatatga aaacctgaaa aaaaaaacaa 2217
137 aaaaaaaaaa 2226
139 <210> SEQ ID NO: 2
140 <211> LENGTH: 317
141 <212> TYPE: PRT
142 <213> ORGANISM: Homo sapiens
144 <400> SEQUENCE: 2
145 Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser Glu
146 1 5 10 15
147 Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His Ala
148 20 25 30
149 Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met
150 35 40 45
151 Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val
152 50 55 60
153 Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser
154 65 70 75 80
155 Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn
156 85 90 95
157 Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile
158 100 105 110
159 Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln
160 115 120 125
161 Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys
162 130 135 140
163 Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu
164 145 150 155 160
165 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro
166 165 170 175
167 Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly
168 180 185 190
169 Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val
170 195 200 205
171 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
172 210 215 220
173 His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val
174 225 230 235 240
175 Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met
176 245 250 255

```

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177 Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe  
 178 260 265 270  
 179 Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu  
 180 275 280 285  
 181 Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp  
 182 290 295 300  
 183 Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp  
 184 305 310 315

186 &lt;210&gt; SEQ ID NO: 3

187 &lt;211&gt; LENGTH: 192

188 &lt;212&gt; TYPE: PRT

189 &lt;213&gt; ORGANISM: Homo Sapiens

191 &lt;400&gt; SEQUENCE: 3

192 Ala Val Gln Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg  
 193 1 5 10 15  
 194 Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg  
 195 20 25 30  
 196 Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr  
 197 35 40 45  
 198 Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His  
 199 50 55 60  
 200 Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys  
 201 65 70 75 80  
 202 Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys  
 203 85 90 95  
 204 Phe Arg His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln  
 205 100 105 110  
 206 Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His  
 207 115 120 125  
 208 Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu  
 209 130 135 140  
 210 Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser  
 211 145 150 155 160  
 212 Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro  
 213 165 170 175  
 214 Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp  
 215 180 185 190

217 &lt;210&gt; SEQ ID NO: 4

218 &lt;211&gt; LENGTH: 181

219 &lt;212&gt; TYPE: PRT

220 &lt;213&gt; ORGANISM: Homo sapiens

222 &lt;400&gt; SEQUENCE: 4

223 Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu  
 224 1 5 10 15  
 225 Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu  
 226 20 25 30  
 227 Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu  
 228 35 40 45  
 229 Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr

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```

230      50      55      60
231 Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu
232 65      70      75      80
233 Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala
234      85      90      95
235 Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys
236      100      105      110
237 Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp
238      115      120      125
239 Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe
240      130      135      140
241 Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro
242 145      150      155      160
243 Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys
244      165      170      175
245 Val Arg Asp Ile Asp
246      180
248 <210> SEQ ID NO: 5
249 <211> LENGTH: 178
250 <212> TYPE: PRT
251 <213> ORGANISM: Homo sapiens
253 <400> SEQUENCE: 5
254 Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala
255 1      5      10      15
256 Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn
257      20      25      30
258 Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp
259      35      40      45
260 Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn
261      50      55      60
262 Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn
263 65      70      75      80
264 Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr
265      85      90      95
266 Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser
267      100      105      110
268 Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn
269      115      120      125
270 Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu
271      130      135      140
272 Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu
273 145      150      155      160
274 Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp
275      165      170      175
276 Ile Asp
279 <210> SEQ ID NO: 6
280 <211> LENGTH: 173
281 <212> TYPE: PRT
282 <213> ORGANISM: Homo sapiens

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/933,915A

DATE: 04/21/2004  
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Input Set : A:\07917-120001.txt  
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Base Note:

Presence of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 4,9,12

**VERIFICATION SUMMARY**

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Input Set : A:\07917-120001.txt

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375 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9

376 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0